This listing of claims will replace all prior versions and listings of claims in the application:

Listing of Claims:

1-18. (Cancelled)

19. (Currently Amended) A method of ~~constructing a library of structurally-constrained peptides~~ identifying peptides capable of binding to a bioactive target molecule comprising

~~preparing library of peptides having a scaffold for β-turn display,~~ a)providing a library of peptides comprising a trpzip scaffold, wherein each peptide comprise~~sing~~ a presented turn sequence and a trpzip scaffold comprising a first and a second opposite strand with a defined backbone hydrogen-bonding pattern, each strand comprising a trpzip domain of at least two Trp residues at non-hydrogen-bonded positions, and each trpzip domain consists of the amino acid sequence WX_1W, wherein X_1 is independently Thr or independently an amino acid selected from the group consisting of H, V, I, F, Y, and W, ~~; and~~ wherein the Trp residues from each trpzip domain form a cross-strand pair without any disulfide bond, wherein the presented turn sequence is flanked by the first and second opposite strands and comprises random amino acids; b)contacting the library with the bioactive target molecule; c) selecting at least one peptide capable of forming a noncovalent complex with the bioactive target molecule from the library; and d) optionally, isolating the at least one selected peptide.

20. (Original) The method of claim 19, wherein the presented turn sequence comprises at least 4 amino acids.

21. (Original) The method of claim 19, wherein the presented turn sequence comprises at least 6 amino acids.

22. (Original) The method of claim 19, wherein each flanking strand consists of naturally occurring L-form amino acids.

23.　　(Original)　The method of claim 19, wherein each flanking strand is at least 3 amino acids in length.

24.　　(Original)　The method of claim 19, wherein each peptide comprises at least 10 amino acids.

25.　　(Cancelled)

26.　　(Currently Amended)　The method of claim ~~25~~ 19, wherein each peptide comprises about 12 amino acids.

27.　　(Currently Amended)　The method of claim ~~25~~ 19, wherein each peptide comprises about 16 amino acids.

28.　　(Cancelled)

29.　　(cancelled)